

In the Specification:

Please amend the paragraph beginning at page 20, line 8 as follows:

B¹
Another aspect of the present invention provides a nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence of nucleotides encoding a F3'H, wherein the translation of the said nucleic acid molecule comprises the amino acid sequence RPPNSGA (SEQ ID NO:43). Preferably, the translation of the said nucleic acid molecule comprises the amino acid sequence RPPNSGAXHXAYNYXDL (SEQ ID NO:44) and still more preferably the translation of the said nucleic acid molecule comprises the amino acid sequence RPPNSGAXHXAYNYXDL[X]_nGGEK (SEQ ID NO:45), where X represents any amino acid and [X]_n represents an amino acid sequence of from 0 to 500 amino acids.

Please amend the paragraph beginning at page 55, line 3 as follows:

B²
The expression of the introduced KC-1 cDNA in the Skr4 x SW63 hybrid had a marked effect on flower colour. Ten of the twelve transgenic plants transformed with pCGP1810 produced flowers with an altered petal colour (RHSCC# 73A), compared with the Skr4 x Sw63 control (RHSCC# 75C). Moreover the anthers and pollen of the transgenic flowers were pink, compared with those of the control Skr4 x SW63 plant, which were white. In addition, expression of the KC-1 cDNA in the Skr4 x SW63 hybrid conferred a dark pink hue to the corolla, which is normally pale lilac. The colour codes are taken from the Royal Horticultural Society's Colour Chart (RHSCC). They provide an alternative means by which to describe the colour phenotypes observed. The designated numbers, however, should be taken only as a guide to the perceived colours and should not be regarded as limiting the possible colours which may be obtained.

Please amend the paragraph beginning at page 79, line 12 as follows:

B3
The nucleotide and predicted amino acid sequences of the rose F3'H #34 cDNA clone (SEQ ID NO:14 and SEQ ID NO:15) were compared with those of the petunia OGR-38 F3'H cDNA clone (SEQ ID NO:1 and SEQ ID NO:2) and the snapdragon sd F3'H clone (SEQ ID NO:5 and SEQ ID NO:6). The rose F3'H #34 cDNA clone showed 64.7% similarity, over 1651 nucleotides and 72.7% similarity, over 509 amino acids, to that of the petunia OGR-38 cDNA clone, and 67.2% similarity, over 1507 nucleotides, and 68.9 similarity, over 502 amino acids, to that of the snapdragon sdF3'H clone.

Please amend the paragraph beginning at page 91, line 7 as follows:

Sub D10
B4
Multiple sequence alignments were performed using the ClustalW program as described in Example 3. Table 7 (below) provides a multiple sequence alignment of the predicted amino acid sequences of petunia OGR-38 (A) (SEQ ID NO:2); carnation (B) (SEQ ID NO:4); snapdragon (C) (SEQ ID NO:6); arabidopsis Tt7 coding region (D) (SEQ ID NO:42); rose (E) (SEQ ID NO:15); chrysanthemum (F) (SEQ ID NO:17); torenia (G) (SEQ ID NO:19); morning glory (H) (SEQ ID NO:21); gentian (partial sequence) (I) (SEQ ID NO:23); lisianthus (partial sequence) (J) (SEQ ID NO:25) and the petunia 651 cDNA (K) (SEQ ID NO:41). Conserved amino acids are shown in bolded capital letters and are boxed and shaded. Similar amino acids are shown in capital letters and are only lightly shaded, and dissimilar amino acids are shown in lower case letters.

In the Sequence Listing:

Please delete the Sequence Listing of record, and substitute the Sequence Listing submitted herewith.